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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/373,658B

DATE: 02/22/2001

TIME: 15:17:28

TECH CENTER 1600/2900 P#15

Input Set : A:\seq\list14881070006.txt

Output Set: N:\CRF3\02222001\I373658B.raw

ENTERED

7 <110> APPLICANT: Iruela-Arispe, Luisa  
 8 Hastings, Gregg A.  
 9 Ruben, Steven M.  
 10 Jonak, Zdenka L.  
 11 Trulli, Stephen H.  
 12 Fronwald, James A.  
 13 Terrett, Jonathan A.  
 16 <120> TITLE OF INVENTION: Meth1 and Meth2 Polynucleotides and Polypeptides  
 19 <130> FILE REFERENCE: 1488.1070006  
 22 <140> CURRENT APPLICATION NUMBER: 09/373,658B  
 25 <141> CURRENT FILING DATE: 1999-08-13  
 28 <160> NUMBER OF SEQ ID NOS: 127  
 31 <170> SOFTWARE: PatentIn Ver. 2.0  
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 38 <213> ORGANISM: Homo sapiens  
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 45 <221> NAME/KEY: misc\_feature  
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 59 <220> FEATURE:  
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 61 <222> LOCATION: (3261)  
 64 <223> OTHER INFORMATION: n is any nucleic acid  
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 68 Met Gly Asn Ala Glu Arg Ala Pro Gly Ser Arg Ser Phe Gly Pro Val  
 69 1 5 10 15  
 71 ccc acg ctg ctg ctg ctc gcc gcg gcg cta ctg gcc gtg tcg gac gca 96  
 72 Pro Thr Leu Leu Leu Leu Ala Ala Ala Leu Leu Ala Val Ser Asp Ala  
 73 20 25 30  
 75 ctc ggg cgc ccc tcc gag gag gac gag gag cta gtg gtg ccg gag ctg 144  
 76 Leu Gly Arg Pro Ser Glu Glu Asp Glu Glu Leu Val Val Pro Glu Leu  
 77 35 40 45  
 79 gag cgc gcc ccg gga cac ggg acc acg cgc ctc cgc ctg cac gcc ttt 192

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81      50      55      60
83 gac cag cag ctg gat ctg gag ctg cgg ccc gac agc agc ttt ttg gcg 240
84 Asp Gln Gln Leu Asp Leu Glu Leu Arg Pro Asp Ser Ser Phe Leu Ala
85 65      70      75      80
87 ccc ggc ttc acg ctc cag aac gtg ggg cgc aaa tcc ggg tcc gag acg 288
88 Pro Gly Phe Thr Leu Gln Asn Val Gly Arg Lys Ser Gly Ser Glu Thr
89      85      90      95
91 ccg ctt ccg gaa acc gac ctg gcg cac tgc ttc tac tcc ggc acc gtg 336
92 Pro Leu Pro Glu Thr Asp Leu Ala His Cys Phe Tyr Ser Gly Thr Val
93      100      105      110
95 aat ggc gat ccc agc tcg gct gcc gcc ctc agc ctc tgc gag ggc gtg 384
96 Asn Gly Asp Pro Ser Ser Ala Ala Ala Leu Ser Leu Cys Glu Gly Val
97      115      120      125
99 cgc ggc gcc ttc tac ctg ctg ggg gag gcg tat ttc atc cag ccg ctg 432
100 Arg Gly Ala Phe Tyr Leu Leu Gly Glu Ala Tyr Phe Ile Gln Pro Leu
101      130      135      140
103 ccc gcc gcc agc gag cgc ctc gcc acc gcc gcc cca ggg gag aag ccg 480
104 Pro Ala Ala Ser Glu Arg Leu Ala Thr Ala Ala Pro Gly Glu Lys Pro
105 145      150      155      160
107 ccg gca cca cta cag ttc cac ctc ctg cgg cgg aat cgg cag ggc gac 528
108 Pro Ala Pro Leu Gln Phe His Leu Leu Arg Arg Asn Arg Gln Gly Asp
109      165      170      175
111 gta ggc ggc acg tgc ggg gtc gtg gac gac gag ccc cgg ccg act ggg 576
112 Val Gly Gly Thr Cys Gly Val Val Asp Asp Glu Pro Arg Pro Thr Gly
113      180      185      190
115 aaa gcg gag acc gaa gac gag gac gaa ggg act gag ggc gag gac gaa 624
116 Lys Ala Glu Thr Glu Asp Glu Asp Glu Gly Thr Glu Gly Glu Asp Glu
117      195      200      205
119 ggg cct cag tgg tcg ccg cag gac ccg gca ctg caa ggc gta gga cag 672
120 Gly Pro Gln Trp Ser Pro Gln Asp Pro Ala Leu Gln Gly Val Gly Gln
121      210      215      220
123 ccc aca gga act gga agc ata aga aag aag cga ttt gtg tcc agt cac 720
124 Pro Thr Gly Thr Gly Ser Ile Arg Lys Lys Arg Phe Val Ser Ser His
125 225      230      235      240
127 cgc tat gtg gaa acc atg ctt gtg gca gac cag tcg atg gca gaa ttc 768
128 Arg Tyr Val Glu Thr Met Leu Val Ala Asp Gln Ser Met Ala Glu Phe
129      245      250      255
131 cac ggc agt ggt cta aag cat tac ctt ctc acg ttg ttt tcg gtg gca 816
132 His Gly Ser Gly Leu Lys His Tyr Leu Leu Thr Leu Phe Ser Val Ala
133      260      265      270
135 gcc aga ttg tac aaa cac ccc agc att cgt aat tca gtt agc ctg gtg 864
136 Ala Arg Leu Tyr Lys His Pro Ser Ile Arg Asn Ser Val Ser Leu Val
137      275      280      285
139 gtg gtg aag atc ttg gtc atc cac gat gaa cag aag ggg ccg gaa gtg 912
140 Val Val Lys Ile Leu Val Ile His Asp Glu Gln Lys Gly Pro Glu Val
141      290      295      300
143 acc tcc aat gct gcc ctc act ctg cgg aac ttt tgc aac tgg cag aag 960
144 Thr Ser Asn Ala Ala Leu Thr Leu Arg Asn Phe Cys Asn Trp Gln Lys

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213	Gly	Gly	Lys	Tyr	Cys	Glu	Gly	Lys	Arg	Val	Arg	Tyr	Arg	Ser	Cys	Asn	
214				580					585					590			
216	ctt	gag	gac	tgt	cca	gac	aat	aat	gga	aaa	acc	ttt	aga	gag	gaa	caa	1824
217	Leu	Glu	Asp	Cys	Pro	Asp	Asn	Asn	Gly	Lys	Thr	Phe	Arg	Glu	Glu	Gln	
218				595				600					605				
220	tgt	gaa	gca	cac	aac	gag	ttt	tca	aaa	gct	tcc	ttt	ggg	agt	ggg	cct	1872
221	Cys	Glu	Ala	His	Asn	Glu	Phe	Ser	Lys	Ala	Ser	Phe	Gly	Ser	Gly	Pro	
222		610					615					620					
224	gcg	gtg	gaa	tgg	att	ccc	aag	tac	gct	ggc	gtc	tca	cca	aag	gac	agg	1920
225	Ala	Val	Glu	Trp	Ile	Pro	Lys	Tyr	Ala	Gly	Val	Ser	Pro	Lys	Asp	Arg	
226	625					630					635				640		
228	tgc	aag	ctc	atc	tgc	caa	gcc	aaa	ggc	att	ggc	tac	ttc	ttc	gtt	ttg	1968
229	Cys	Lys	Leu	Ile	Cys	Gln	Ala	Lys	Gly	Ile	Gly	Tyr	Phe	Phe	Val	Leu	
230				645					650					655			
232	cag	ccc	aag	gtt	gta	gat	ggg	act	cca	tgt	agc	cca	gat	tcc	acc	tct	2016
233	Gln	Pro	Lys	Val	Val	Asp	Gly	Thr	Pro	Cys	Ser	Pro	Asp	Ser	Thr	Ser	
234				660				665					670				
236	gtc	tgt	gtg	caa	gga	cag	tgt	gta	aaa	gct	ggg	tgt	gat	cgc	atc	ata	2064
237	Val	Cys	Val	Gln	Gly	Gln	Cys	Val	Lys	Ala	Gly	Cys	Asp	Arg	Ile	Ile	
238		675				680					685						
240	gac	tcc	aaa	aag	aag	ttt	gat	aaa	tgt	ggg	gtt	tgc	ggg	gga	aat	gga	2112
241	Asp	Ser	Lys	Lys	Lys	Phe	Asp	Lys	Cys	Gly	Val	Cys	Gly	Gly	Asn	Gly	
242		690				695					700						
244	tct	act	tgt	aaa	aaa	ata	tca	gga	tca	gtt	act	agt	gca	aaa	cct	gga	2160
245	Ser	Thr	Cys	Lys	Lys	Ile	Ser	Gly	Ser	Val	Thr	Ser	Ala	Lys	Pro	Gly	
246	705					710					715				720		
248	tat	cat	gat	atc	atc	aca	att	cca	act	gga	gcc	acc	aac	atc	gaa	gtg	2208
249	Tyr	His	Asp	Ile	Ile	Thr	Ile	Pro	Thr	Gly	Ala	Thr	Asn	Ile	Glu	Val	
250				725						730				735			
253	aaa	cag	cgg	aac	cag	agg	gga	tcc	agg	aac	aat	ggc	agc	ttt	ctt	gcc	2256
254	Lys	Gln	Arg	Asn	Gln	Arg	Gly	Ser	Arg	Asn	Asn	Gly	Ser	Phe	Leu	Ala	
255			740					745				750					
257	atc	aaa	gct	gct	gat	ggc	aca	tat	att	ctt	aat	ggg	gac	tac	act	ttg	2304
258	Ile	Lys	Ala	Ala	Asp	Gly	Thr	Tyr	Ile	Leu	Asn	Gly	Asp	Tyr	Thr	Leu	
259			755					760				765					
261	tcc	acc	tta	gag	caa	gac	att	atg	tac	aaa	ggg	gtt	gtc	ttg	agg	tac	2352
262	Ser	Thr	Leu	Glu	Gln	Asp	Ile	Met	Tyr	Lys	Gly	Val	Val	Leu	Arg	Tyr	
263		770				775					780						
265	agc	ggc	tcc	tct	gcg	gca	ttg	gaa	aga	att	cgc	agc	ttt	agc	cct	ctc	2400
266	Ser	Gly	Ser	Ser	Ala	Ala	Leu	Glu	Arg	Ile	Arg	Ser	Phe	Ser	Pro	Leu	
267	785					790					795				800		
269	aaa	gag	ccc	ttg	acc	atc	cag	gtt	ctt	act	gtg	ggc	aat	gcc	ctt	cga	2448
270	Lys	Glu	Pro	Leu	Thr	Ile	Gln	Val	Leu	Thr	Val	Gly	Asn	Ala	Leu	Arg	
271				805						810				815			
273	cct	aaa	att	aaa	tac	acc	tac	ttc	gta	aag	aag	aag	aag	gaa	tct	ttc	2496
274	Pro	Lys	Ile	Lys	Tyr	Thr	Tyr	Phe	Val	Lys	Lys	Lys	Lys	Glu	Ser	Phe	
275				820					825					830			
277	aat	gct	atc	ccc	act	ttt	tca	gca	tgg	gtc	att	gaa	gag	tgg	ggc	gaa	2544

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281 tgt tct aag tca tgt gaa ttg ggt tgg cag aga aga ctg gta gaa tgc 2592
282 Cys Ser Lys Ser Cys Glu Leu Gly Trp Gln Arg Arg Leu Val Glu Cys
283      850      855      860
285 cga gac att aat gga cag cct gct tcc gag tgt gca aag gaa gtg aag 2640
286 Arg Asp Ile Asn Gly Gln Pro Ala Ser Glu Cys Ala Lys Glu Val Lys
287 865      870      875      880
289 cca gcc agc acc aga cct tgt gca gac cat ccc tgc ccc cag tgg cag 2688
290 Pro Ala Ser Thr Arg Pro Cys Ala Asp His Pro Cys Pro Gln Trp Gln
291      885      890      895
293 ctg ggg gag tgg tca tca tgt tct aag acc tgt ggg aag ggt tac aaa 2736
294 Leu Gly Glu Trp Ser Ser Cys Ser Lys Thr Cys Gly Lys Gly Tyr Lys
295      900      905      910
297 aaa aga agc ttg aag tgt ctg tcc cat gat gga ggg gtg tta tct cat 2784
298 Lys Arg Ser Leu Lys Cys Leu Ser His Asp Gly Gly Val Leu Ser His
299      915      920      925
301 gag agc tgt gat cct tta aag aaa cct aaa cat ttc ata gac ttt tgc 2832
302 Glu Ser Cys Asp Pro Leu Lys Lys Pro Lys His Phe Ile Asp Phe Cys
303      930      935      940
305 aca atg gca gaa tgc agt taa gtggtttaag tgggtgtagc tttgaggcaa 2883
306 Thr Met Ala Glu Cys Ser
307 945      950
309 ggcaaagtga ggaagggctg gtgcagggaa agcaagaagg ctggagggat ccagcgtatc 2943
311 ttgccagtaa ccagtggagt gtatcagtaa ggtgggatta tgggggtaga tagaaaagga 3003
313 gttgaatcat cagagtaaac tgccagttgc aaatttgata ggatagttag tgaggattat 3063
W--> 316 taacctctga gcagtgatat agcataataa anccccgggc attattatta ttatttcttt 3123
318 tgttacatct attacaagtt tagaaaaaac aaagcaattg tcaaaaaaaaa aaaaaaaaaa 3183
320 aaaaaaaaaa aaggggcggc cgctctagag gatccctoga ggggcccaag cttacgcgtg 3243
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336 Pro Thr Leu Leu Leu Leu Ala Ala Ala Leu Leu Ala Val Ser Asp Ala
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339 Leu Gly Arg Pro Ser Glu Glu Asp Glu Glu Leu Val Val Pro Glu Leu
340 35 40 45
342 Glu Arg Ala Pro Gly His Gly Thr Thr Arg Leu Arg Leu His Ala Phe
343 50 55 60
345 Asp Gln Gln Leu Asp Leu Glu Leu Arg Pro Asp Ser Ser Phe Leu Ala
346 65 70 75 80
348 Pro Gly Phe Thr Leu Gln Asn Val Gly Arg Lys Ser Gly Ser Glu Thr
349 85 90 95
351 Pro Leu Pro Glu Thr Asp Leu Ala His Cys Phe Tyr Ser Gly Thr Val
352 100 105 110

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**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

## VERIFICATION SUMMARY

DATE: 02/22/2001

PATENT APPLICATION: US/09/373,658B

TIME: 15:17:30

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L:1548 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14  
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L:1645 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:1647 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
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L:10055 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50  
L:10057 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50

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